AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows: .

Please delete the paragraph beginning on page 8 spanning lines 9-16 and replace it with the following paragraph:

FIGS. 1A and 1B – Schematic representation of the screening protocol. The assay is carried out as described in Zhang et al. (Zhang et al., 2000). Two plasmids, depicted graphically in FIG. 1A., are transformed into *E. coli.* one encodes the lambda repressor DNA-binding domain (DBD) fused to a target epitope (SEQ ID NO:5 AND SEQ ID NO:3). The other encodes the DBD fused to a peptide library. As shown in FIG. 1B., cells that contain library-encoded peptides (LEPs) that bind the target epitope, reconstitute the otherwise weak DNA-binding activity of the lambda Repressor DBD. This renders these cells immune to phage lambda infection, allowing them to be selected form the population.

Please delete the paragraph beginning on page 8 spanning lines 9-16 and replace it with the following paragraph:

FIG. 3 – Scheme for purification of a recombinant protein based on a peptide-peptide interaction. The yeast Gal80 protein was fused to two tags, six histidine and LEPB (a 15-mer selected to bind a 14-mer called ICS using the system shown in FIGS. 1A-B). This protein was expressed in *E. coli.* A crude extract was split and applied either to a standard Ni-NTA agarose resin (Qiagen) or to synthetic ICS peptide immobilized covalently on Affi-gel. The ICS peptide column provided a high level of purity of the LEPB-tagged protein (LEPB=KARKEAELAAATAEQ(SEQ ID NO:1).

Please delete the paragraph beginning on page 8 spanning lines 29-31 and continuing on page 9 spanning lines 1-7 and replace it with the following paragraph:

FIG. 5 - "Far Western" blot protocol to eliminate false positives. An extract is prepared from phage-resistant cells that express the DBD-LEP fusion. This is electrophoresed through a denaturing gel, then blotted onto a membrane. This is probed with a GST fusion

protein containing the target epitope, followed by labeled anti-GST antibody to visualize the site(s) of binding of the GST-peptide fusion protein. In this case, two of the four selected peptides provided strong signals, showing that they are true hits, while two (LEPC and LEPD, provided weak or unobservable signals, indicating that they are false positives, or binding peptides that associate too weakly to be of practical utility. LEPA = Large (40 kD) polypeptide; LEPB = KARKEAELAAATAEQ ~~(SEQ ID NO:2)~~(SEQ ID NO:1); LEPC = PCP; LEPD = PCHLNCSLQTLSPTRTTPRKHCKHCFKTLSEKMKWN ~~(SEQ ID NO:3)~~(SEQ ID NO:2).

Please delete the paragraph beginning on page 9 spanning lines 14-19 and replace it with the following paragraph:

FIG. 8 - Schematic diagram of a substrate-targeted protease inhibitor. This would be a novel application of EBMs capable of binding an epitope containing a protease cleavage site. Unlike common protease inhibitors, they could block processing of one, but not all, substrates of a particular enzyme. The same approach could theoretically be applied to the inhibition of phosphorylation events, ubiquitination and many other protein post-translational modifications (SEQ ID NO:3).

Please delete the paragraph beginning on page 9 spanning lines 20-26 and replace it with the following paragraph:

FIG. 9 - Experimental demonstration of substrate-targeted inhibition of proteolysis using an epitope-binding peptide (LEPB). The experiment shown schematically in FIG. 5 was carried out. Addition of increasing amounts of LEPB to a reaction containing a protease and two different substrates inhibited one cleavage event, but not the other. Only the substrate containing the epitope recognized by LEPB was protected from cleavage. GG = GSTNEAYVHDGPVRSLNGFP (SEQ ID NO:3); GM = GSTGVVWFKDSVGVSGNMBP (SEQ ID NO:4); LEPB = KARKEAELAAATAEQ (SEQ ID NO:1).